Recurrent Selection on the Winters Sex-ratio Genes in Drosophila Simulans

TABLE 1

Population genetic summary statistics

	n (n_{anc})	L	S	π	θ_W	h	Z_NS	TD	FWH
Dox									
All Data	71	2342	155	0.00509	0.01396	6***	0.52**	-2.19***	-25.95
Population									
Nicewicz	12 (0)	5521	19	0.00057	0.00114	4*	0.80**	-2.17**	--
Tremont	34 (0)	5956	12	0.00045	0.00049	7	0.35	-0.29	0.06
Winters	12 (0)	60601	8	0.0004	0.00044	3	0.76*	-0.34	--
Africa	5 (2)	2343	116	0.02945	0.02376	3*	0.97**	1.82*	-1.20
Allele									
Derived	67	5511	22	0.00044	0.00084	8*	0.31	-1.48*	0.03
Ancestral	4	2388	84	0.01982	0.01919	4	0.5	0.35	2.33
MDox									
All Data	69	2788	118	0.0023	0.00918	10***	0.32*	-2.58***	-24.57
Population									
Nicewicz	12 (0)	4401	12	0.00045	0.0009	3*	0.83*	-2.09***	0.15
Tremont	33 (0)	4507	9	0.00017	0.00049	5	0.25	-1.98**	0.18
Winters	12 (0)	4508	1	0.00004	0.00007	2	--	-1.14*	0.15
Africa	5 (3)	2788	103	0.01772	0.01859	4	0.37	-0.36	6.40
Allele									
Derived	65	4400	18	0.00018	0.00086	8	0.26	-2.40***	0.15
Ancestral	4	2815	92	0.01812	0.0186	4	0.41	-0.27	4.33
Nmy									
All Data	115	5335	155	0.0009	0.00553	11***	0.40*	-2.76***	-91.63***
Population									
Nicewicz	24 (0)	7461	0	0	0	1	--	--	--
Tremont	66 (1)	5403	60	0.00034	0.00233	7***	0.84***	-2.88***	-36.19**
Winters	12 (1)	5385	121	0.00374	0.00744	2***	1.00***	-2.32**	-72.88***
Africa	5 (0)	7311	60	0.00372	0.00359	4***	0.47	0.315	-3.50
Allele									
Derived	113	7310	67	0.00028	0.00179	11***	0.41**	-2.69***	-29.72**

Ancestral	2	5402	66	0.01222	0.01222	2	1.00	--	--

n is the number of chromosomes sampled. n_{anc} is the number of ancestral alleles present in each population sample. *L* is the total number of sites analyzed, excluding alignment gaps. *S* is the number of segregating sites. *h* is the number of haplotypes. π is the average number of pairwise differences (Nei 1987). θ_W is Watterson's estimator of population diversity (Watterson, 1975). $Z_N S$ is the average pairwise R^2 (Kelley 1997). *TD* is Tajima's D (Tajima 1989). *FWH* is Fay and Whu's H (Fay and Wu 2000). * indicates $P < 0.05$, ** indicates $P < 0.01$, *** indicates $P < 0.001$.

TABLE 2

Prior distributions of parameters for selection model

	Dox			***MDox***			***Nmy***		
	prior	*mean*	*95% density*	*prior*	*mean*	*95% density*	*prior*	*mean*	*95% density*
μ	Gam(10^{-10},12)	1.2×10^{-9}	6.3×10^{-10}-2.0×10^{-9}	Gam(10^{-10},12)	1.2×10^{-9}	6.3×10^{-10}-2.0×10^{-9}	Gam(10^{-10},10)	1.0×10^{-9}	4.8×10^{-10}-1.7×10^{-9}
r	Gam(10^{-10},48)	4.8×10^{-9}	3.5×10^{-9}-6.3×10^{-9}	Gam(10^{-10},48)	4.8×10^{-9}	3.5×10^{-9}-6.3×10^{-9}	Gam(10^{-10},82)	8.2×10^{-9}	6.5x10-^{9}-10x10-^{9}
N	Gam(4×10^{4},25)	1.0×10^{6}	6.5×10^{5}-1.4×10^{6}	Gam(4×10^{4},25)	1.0×10^{6}	6.5×10^{5}-1.4×10^{6}	Gam(1×10^{5},25)	2.5×10^{6}	1.6×10^{6}-3.7×10^{6}
s	U(5×10^{-4},0.5)	--	--	U(5×10^{-4},0.5)	--	--	U(5×10^{-4},0.5)	--	--
θ	--	30	4.9-110	--	22	3.6-80	--	75	9.7-320
ρ	--	120	35-330	--	87	25-240	--	610	160-1540

μ is the per site mutation rate. *r* is the per site recombination rate. *N* is the effective population size. *s* is the selection coefficient. θ is the per locus population mutation parameter, ρ is the per locus population recombination parameter.

TABLE 3
HKA Tests

Gene	Population	Chromosome	*L*	*n*	*S*	*Div*	χ^2	*P*-value
Winters *SR* Data								
Dox	Nicewicz	X	5521	12	19	0.0567	52.51	<0.0001
Dox	Tremont	X	5956	34	12	0.0567	93.27	<0.0001
Dox	Winters	X	6061	12	8	0.0567	72.17	<0.0001
MDox	Nicewicz	X	4401	12	12	0.0611	41.22[b]	<0.0001
MDox	Tremont	X	4507	33	9	0.0611	59.31	<0.0001
MDox	Winters	X	4508	12	1	0.0611	49.72	<0.0001
Nmy	Nicewicz	3R	7461	24	0	0.0516	77.34	<0.0001
Nmy	Tremont	3R	7460	65	0	0.0516	94.52	<0.0001
Nmy	Winters	3R	7461	11	1	0.0516	59.92	<0.0001
NmyAll[a]	Tremont	3R	5403	66	60	0.0513	42.85	<0.0001
NmyAll	Winters	3R	5385	12	121	0.0511	20.28	0.0903
Begun and Whitley (2000) Data								
bnb	Winters	X	1015	8	11	0.0197	17.99	0.0764
mei-218	Winters	X	1187	8	14	0.0687		
ovo	Winters	X	1356	8	9	0.0270		
sn	Winters	X	1437	8	28	0.0370		
sog	Winters	X	1233	8	8	0.0251		
X	Winters	X	1425	8	24	0.0281		
yp3	Winters	X	1227	8	8	0.0473		
AP-50	Winters	3R	1398	8	58	0.0293		
fzo	Winters	3R	1360	8	22	0.0708		
hyd	Winters	3R	1786	8	26	0.0208		
Osbp	Winters	3R	1166	8	31	0.0266		
ry	Winters	3R	1362	8	54	0.0419		
T-cp1	Winters	3R	1201	8	9	0.0325		

L is the number of bases sequenced in *D. simulans*. *n* is the number of *D. simulans* chromosomes sampled. *S* is the number of segregating sites. *Div* is the per-base divergence from *D. melanogaster*. χ^2 and *P* values correspond to multi-locus HKA tests on 13 loci previously sequenced in *D. simulans* (bottom) and when data from single Winters *SR* genes for each North American population were added to the 13 loci (top). See text for details. [a]. Ancestral alleles were not excluded from the analysis (Nicewicz has no ancestral alleles in sample).

TABLE 4

Posteriors distribution of parameters for selection model

		Dox		*MDox*		*Nmy*	
Nicewicz		**median**	**95% CI**	**median**	**95% CI**	**median**	**95% CI**
	T (N gen)	0.0348	0.0064-0.112	0.0308	0.0037-0.112		
	T (years)	3,500	610-10,000	2,900	330-11,000		
	θ	28	15-49	20	11-35		
	ρ	120	70-180	86	52-130		
	s	0.063	0.0019-0.46	0.063	0.0015-0.46		
Tremont							
	T (N gen)	0.0312	0.0072-0.156	0.0304	0.0040-0.104	0.0068	0.0020-0.0212
	T (years)	2,900	760-12,000	2,800	360-9,700	1,600	550-4,500
	θ	21	9.6-43	17	8.9-32	61	29-130
	ρ	110	63-170	83	50-130	560	340-850
	s	0.1	0.0023-0.48	0.055	0.0017-0.47	0.28	0.014-0.49
Winters							
	T (N gen)	0.034	0.0035-0.136	0.0328	0.0040-0.148	0.0164	0.0032-0.064
	T (years)	3,200	300-12,000	3,100	400-14,000	3,800	790-14,000
	θ	22	11-42	18	8.5-36	59	26-120
	ρ	110	68-180	81	49-133	570	340-890
	s	0.059	0.0021-0.48	0.26	0.021-0.48	0.27	0.023-0.49

T (N gen) is the time since selection in coalescent time units. T (years) is the time since selection in years. θ is the per-locus population mutation rate. ρ is the per-locus population recombination rate. s is the selection coefficient. 95% CI is the 95% credible interval.

SUPPLEMENTARY TABLE 1

Geographic Distribution of Ancestral and Derived Alleles

North American Populations		**Number of ancestral alleles (total sampled)**		
Geographic Origin	**Population Name**	***Dox***	***MDox***	***Nmy***
Bolton, MA	Nicewicz	0 (12)	0 (12)	0 (24)
Cambridge, MA	Tremont	0 (34)	0 (33)	1 (66)
Winters, CA	Winters	0 (12)	0 (12)	1 (12)

Global Panel				
Geographic Origin	**Stock ID**	***Dox* Allele**	***MDox* Allele**	***Nmy* Allele**
Madagascar	14021.0251.196	ancestral	ancestral	derived
	14021.0251.197	ancestral	ancestral	derived
Kenya	14021.0251.199	derived	ancestral	derived
Congo	14021.0251.184	derived	derived	derived
South Africa	14021.0251.169	derived	derived	derived
California	14021.0251.194	derived	derived	derived
North America, unknown	14021.0251.195	derived	derived	derived
Scotland	14021.0251.216	derived	derived	derived
Greece	14021.0251.181	derived	derived	derived
New Guinea	14021.0251.009	derived	derived	derived
New Zealand	14021.0251.007	ancestral	ancestral	derived
Australia	14021.0251.176	derived	derived	derived
New Caledonia	14021.0251.198	ancestral	derived	derived

SUPPLEMENTARY TABLE 2

Begun and Whitley 2000 loci Complete sequence. Winters, CA populations

Locus	Chromosome	*n*	*L*	*S*	*h*	π	θ_W	*TD*	ρ
Aats-gluprop	3R	6	1348	32	6	0.0101	0.0110	-0.5508	0.0367
AP-50	3R	8	1398	58	7	0.0161	0.0166	-0.1578	0.0360
Cen190	3R	7	1287	23	4	0.0091	0.0073	1.4001	0.0093
fzo	3R	8	1362	22	5	0.0068	0.0062	0.4938	0.0041
Hsc70	3R	7	1292	10	6	0.0031	0.0032	-0.1073	0.0271
hyd	3R	8	1793	26	7	0.0057	0.0056	0.0794	0.0000
miranda	3R	5	1200	29	5	0.0113	0.0120	-0.4673	0.8265
nos	3R	7	1073	20	7	0.0074	0.0078	-0.2433	0.0096
Osbp	3R	8	1167	31	7	0.0101	0.0103	-0.0914	0.1235
oso	3R	7	971	24	5	0.0107	0.0101	0.3380	0.0092
pit	3R	7	1267	52	5	0.0196	0.0179	0.5476	0.0333
ry	3R	8	1362	54	7	0.0163	0.0164	-0.0374	0.0088
T-cp1	3R	8	1201	9	6	0.0028	0.0029	-0.1608	0.0257
tld	3R	7	1013	40	7	0.0189	0.0169	0.6559	0.0305
MEAN						**0.0106**	**0.0103**	**0.1213**	**0.0843**
bnb	X	8	1030	11	6	0.0035	0.0042	-0.8319	0.0000
ct	X	6	1090	2	3	0.0008	0.0008	-0.0500	0.0298
dec-1	X	7	1493	23	5	0.0068	0.0063	0.3685	0.0163
garnet	X	7	1265	17	3	0.0039	0.0055	-1.6704	0.0000
mei-218	X	8	1230	14	4	0.0058	0.0046	1.4083	0.0111
mei-9	X	7	890	6	4	0.0029	0.0028	0.2540	0.0000
otu	X	6	1162	29	5	0.0125	0.0109	0.9132	0.0220
ovo	X	8	1359	9	6	0.0029	0.0026	0.5952	0.0174
pgd	X	7	912	17	3	0.0091	0.0076	1.0809	0.0024
r	X	6	1198	9	4	0.0032	0.0033	-0.1132	0.0451
sn	X	8	1450	28	5	0.0088	0.0078	0.6903	0.0109
sog	X	8	1233	8	5	0.0021	0.0025	-0.8615	0.1266
sqh	X	7	777	10	3	0.0055	0.0053	0.1431	0.0022
X	X	8	1425	24	5	0.0082	0.0065	1.3544	0.0071
yp3	X	8	1241	8	4	0.0027	0.0025	0.2580	0.0011
MEAN						**0.0052**	**0.0049**	**0.2359**	**0.0195**

n is the number of chromosomes sampled. *L* is the length of sequence in base pairs. *S* is the number of segregating sites. *h* is the number of haplotypes. π is the per site average number of pairwise differences (Nei 1987). θ_W is the per site Watterson's estimator of population diversity (Watterson, 1975). *TD* is Tajima's *D* (Tajima 1989). ρ is the per site population recombination rate (Hudson 1987).

SUPPLEMENTARY TABLE 3

	genotype	number of males tested	mean *k* (s.d)
1	*Dox; nmy*	18	0.96 (0.038)
2	*dox[del105]; nmy*	18	0.53 (0.050)
3	*dox[del150]; nmy*	19	0.56 (0.061)
4	*dox[del150]; nmy*	19	0.52 (0.032)
5	*dox[del150]; nmy*	17	0.53 (0.057)

k is the proportion of female progeny.